



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

Elmore et al

Atty. Ref.: 1498-133

Serial No. 08/981,087

Group: 1647

Filed: May 27, 1998

Examiner: Turner

For: TYPE F BOTULINUM TOXIN AND USE THEREOF

* * * * *

January 28, 2003

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

STATEMENT

The attached paper and computer readable copies of the Sequence Listing are the same. No new matter has been added.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____

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NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):



- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☒ 7. Other: Figure 3 see below

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Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

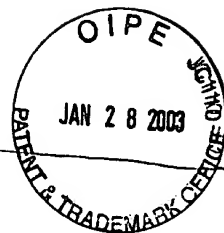
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Elmore, Michael J.
Mauchline, Margaret L.
Minton, Nigel P.
Pasechnik, Vladimir A.
Titball, Richard W.
- (ii) TITLE OF INVENTION: TYPE F BOTULINUM TOXIN AND USE THEREOF
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: NIXON & VANDERHYE P.C.
(B) STREET: 1100 North Glebe Rd. 8th floor
(C) CITY: Arlington
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22201-4741
- #2 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/981,087
(B) FILING DATE: 27-MAY-1998
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/GB96/01409
(B) FILING DATE: 12-JUN-1996
- (viii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: GB 9511909.5
(B) FILING DATE: 12-JUN-1995
- (ix) ATTORNEY/AGENT INFORMATION:
(A) NAME: Crawford, Arthur R.
(B) REGISTRATION NUMBER: 25,327
(C) REFERENCE/DOCKET NUMBER: 124-688
- (x) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-816-4000
(B) TELEFAX: 703-816-4100

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 431 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
1 5 10 15
Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
20 25 30
Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
35 40 45
Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
50 55 60
Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
65 70 75 80
Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
85 90 95
Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
100 105 110
Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
115 120 125
Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
130 135 140
Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
145 150 155 160
Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
165 170 175
Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
180 185 190
Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
195 200 205
Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
210 215 220
Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
225 230 235 240
Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
245 250 255

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Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn
 260 265 270
 Ser Asn Phe Leu Asn Ile Asn Gln Gln Arg Gly Val Tyr Gln Lys Pro
 275 280 285
 Asn Ile Phe Ser Asn Thr Arg Leu Tyr Thr Gly Val Glu Val Ile Ile
 290 295 300
 Arg Lys Asn Gly Ser Thr Asp Ile Ser Asn Thr Asp Asn Phe Val Arg
 305 310 315 320
 Lys Asn Asp Leu Ala Tyr Ile Asn Val Val Asp Arg Asp Val Glu Tyr
 325 330 335
 Arg Leu Tyr Ala Asp Ile Ser Ile Ala Lys Pro Glu Lys Ile Ile Lys
 340 345 350
 Leu Ile Arg Thr Ser Asn Ser Asn Asn Ser Leu Gly Gln Ile Ile Val
 355 360 365
 Met Asp Ser Ile Gly Asn Asn Cys Thr Met Asn Phe Gln Asn Asn Asn
 370 375 380
 Gly Gly Asn Ile Gly Leu Leu Gly Phe His Ser Asn Asn Leu Val Ala
 385 390 395 400
 Ser Ser Trp Tyr Tyr Asn Asn Ile Arg Lys Asn Thr Ser Ser Asn Gly
 405 410 415
 Cys Phe Trp Ser Phe Ile Ser Lys Glu His Gly Trp Gln Glu Asn
 420 425 430

H2

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ser Tyr Thr Asn Asp Lys Ile Leu Ile Leu Tyr Phe Asn Lys Leu Tyr
 1 5 10 15
 Lys Lys Ile Lys Asp Asn Ser Ile Leu Asp Met Arg Tyr Glu Asn Asn
 20 25 30
 Lys Phe Ile Asp Ile Ser Gly Tyr Gly Ser Asn Ile Ser Ile Asn Gly
 35 40 45

Asp Val Tyr Ile Tyr Ser Thr Asn Arg Asn Gln Phe Gly Ile Tyr Ser
 50 55 60
 Ser Lys Pro Ser Glu Val Asn Ile Ala Gln Asn Asn Asp Ile Ile Tyr
 65 70 75 80
 Asn Gly Arg Tyr Gln Asn Phe Ser Ile Ser Phe Trp Val Arg Ile Pro
 85 90 95
 Lys Tyr Phe Asn Lys Val Asn Leu Asn Asn Glu Tyr Thr Ile Ile Asp
 100 105 110
 Cys Ile Arg Asn Asn Asn Ser Gly Trp Lys Ile Ser Leu Asn Tyr Asn
 115 120 125
 Lys Ile Ile Trp Thr Leu Gln Asp Thr Ala Gly Asn Asn Gln Lys Leu
 130 135 140

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Val Phe Asn Tyr Thr Gln Met Ile Ser Ile Ser Asp Tyr Ile Asn Lys
 1 5 10 15
 Trp Ile Phe Val Thr Ile Thr Asn Asn Arg Leu Gly Asn Ser Arg Ile
 20 25 30
 Tyr Ile Asn Gly Asn Leu Ile Asp Glu Lys Ser Ile Ser Asn Leu Gly
 35 40 45
 Asp Ile His Val Ser Asp Asn Ile Leu Phe Lys Ile Val Gly Cys Asn
 50 55 60
 Asp Thr Arg Tyr Val Gly Ile Arg Tyr Phe Lys Val Phe Asp Thr Glu
 65 70 75 80
 Leu Gly Lys Thr Glu Ile Glu Thr Leu Tyr Ser Asp Glu Pro Asp Pro
 85 90 95
 Ser Ile Leu Lys Asp Phe Trp Gly Asn Tyr Leu Leu Tyr Asn Lys Arg
 100 105 110
 Tyr Tyr Leu Leu Asn Leu Leu Arg Thr Asp Lys Ser Ile Thr Gln Asn

	115		120		125										
Ser	Asn	Phe	Leu	Asn	Ile	Asn	Gln	Gln	Arg	Gly	Val	Tyr	Gln	Lys	Pro
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Asn	Ile	Phe	Ser	Asn	Thr	Arg	Leu	Tyr	Thr	Gly	Val	Glu	Val	Ile	Ile
1				5					10					15	
Arg	Lys	Asn	Gly	Ser	Thr	Asp	Ile	Ser	Asn	Thr	Asp	Asn	Phe	Val	Arg
		20						25					30		
Lys	Asn	Asp	Leu	Ala	Tyr	Ile	Asn	Val	Val	Asp	Arg	Asp	Val	Glu	Tyr
	35						40					45			
Arg	Leu	Tyr	Ala	Asp	Ile	Ser	Ile	Ala	Lys	Pro	Glu	Lys	Ile	Ile	Lys
	50					55					60				
Leu	Ile	Arg	Thr	Ser	Asn	Ser	Asn	Asn	Ser	Leu	Gly	Gln	Ile	Ile	Val
65				70					75					80	
Met	Asp	Ser	Ile	Gly	Asn	Asn	Cys	Thr	Met	Asn	Phe	Gln	Asn	Asn	Asn
				85					90					95	
Gly	Gly	Asn	Ile	Gly	Leu	Leu	Gly	Phe	His	Ser	Asn	Asn	Leu	Val	Ala
		100						105					110		
Ser	Ser	Trp	Tyr	Tyr	Asn	Asn	Ile	Arg	Lys	Asn	Thr	Ser	Ser	Asn	Gly
		115						120				125			
Cys	Phe	Trp	Ser	Phe	Ile	Ser	Lys	Glu	His	Gly	Trp	Gln	Glu	Asn	
	130						135					140			

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCATATACTA ATGATAAAAT TCTAATTTTA TATTTTAATA AATTATATAA AAAAATTAAA 60
GATAACTCTA TTTTAGATAT GCGATATGAA AATAATAAAT TTATAGATAT CTCTGGATAT 120
GGTTCAAATA TAAGCATTAA TGGAGATGTA TATATTTATT CAACAAATAG AAATCAATTT 180
GGAATATATA GTAGTAAGCC TAGTGAAGTT AATATAGCTC AAAATAATGA TATTATATAC 240
AATGGTAGAT ATCAAAATTT TAGTATTAGT TTCTGGGTAA GGATTCCTAA ATACTTCAAT 300
AAAGTGAATC TTAATAATGA ATATACTATA ATAGATTGTA TAAGGAATAA TAATTCAGGA 360
TGGAAAATAT CACTTAATTA TAATAAAATA ATTTGGACTT TACAAGATAC TGCTGGAAAT 420
AATCAAAAAC TAGTTTTTAA TTATACACAA ATGATTAGTA TATCTGATTA TATAAATAAA 480
TGGATTTTTG TAACTATTAC TAATAATAGA TTAGGCAATT CTAGAATTTA CATCAATGGA 540
AATTTAATAG ATGAAAAATC AATTTCGAAT TTAGGTGATA TTCATGTTAG TGATAATATA 600
TTATTTAAAA TTGTTGGTTG TAATGATACA AGATATGTTG GTATAAGATA TTTTAAAGTT 660
TTTGATACGG AATTAGGTAA AACAGAAATT GAGACTTTAT ATAGTGATGA GCCAGATCCA 720
AGTATCTTAA AAGACTTTTG GGGAAATTAT TTGTTATATA ATAAAAGATA TTATTTATTG 780
AATTTACTAA GAACAGATAA GTCTATTACT CAGAATTCAA ACTTTCTAAA TATTAATCAA 840
CAAAGAGGTG TTTATCAGAA ACCAAATATT TTTTCCAACA CTAGATTATA TACAGGAGTA 900
GAAGTTATTA TAAGAAAAAA TGGATCTACA GATATATCTA ATACAGATAA TTTTGTTAGA 960
AAAAATGATC TGGCATATAT TAATGTAGTA GATCGTGATG TAGAATATCG GCTATATGCT 1020
GATATATCAA TTGCAAAACC AGAGAAAATA ATAAAATTAA TAAGAACATC TAATTCAAAC 1080
AATAGCTTAG GTCAAATTAT AGTTATGGAT TCAATAGGAA ATAATTGCAC AATGAATTTT 1140
CAAAACAATA ATGGGGGCAA TATAGGATTA CTAGGTTTTT ATTCAAATAA TTTGTTGCT 1200
AGTAGTTGGT ATTATAACAA TATACGAAAA AATACTAGCA GTAATGGATG CTTTTGGAGT 1260
TTTATTTCTA AAGAGCATGG ATGGCAAGAA AAC 1293

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGATCCATAT GTCTTACACT AACGACAAAA TCCTGATCCT GTACTTCAAC AAAGTGTACA 60
AAAAAATCAA AGACAACTCT ATCCTGGACA TCGGTTACGA AAACAACAAA TTCATCGACA 120
TCTCTGGCTA TGGTTCTAAC ATCTCTATCA ACGGTGACGT CTACATCTAC TCTACTAACC 180
GCAACCAGTT CGGTATCTAC TCTTCTAAAC CGTCTGAAGT AAACATCGCT CAGAACAACG 240
ACATCATCTA CAACGGTCGT TACCAGAACT TCTCTATCTC TTTCTGGGTT CGTATCCCGA 300
AATACTTCAA CAAAGTTAAC CTGAACAACG AATACACTAT CATCGACTGC ATCCGTAACA 360
ACAAGTCTGG TTGGAATAAT TCTCTGAAGT ACAACAAAAT CATCTGGACT CTGCAGGACA 420
42 CTGCTGGTAA CAACCAGAAA CTGGTTTTCA ACTACTCTCA GATGATCTCT ATCTCTGACT 480
ACATTAATAA ATGGATCTTC GTTACTATCA CTAACAACCG TCTGGGTAAC TCTCGTATCT 540
ACATCAACGG TAACCTGATC GATGAAAAAT CTATCTCTAA CCTGGGTGAC ATCCACGTTT 600
CTGACAACAT CCTGTTCAAA ATCGTTGGTT GCAACGACAC GCGTTACGTT GGTATCCGTT 660
ACTTCAAAGT TTTGACACT GAACTGGGTA AAAGTGAAT CGAACTCTG TACTCTGACG 720
AACCAGACCC GTCTATCTCG AAAGACTTCT GGGGTAACCTA CCTGCTGTAC AACAAACGTT 780
ACTACCTGCT GAACCTGCTC CGGACTGACA AATCTATCAC TCAGAACTCT AACTTCCTGA 840
ACATCAACCA GCAGCGTGGT GTTTATCAGA AACCTAATAT CTTCTCTAAC ACTCGTCTGT 900
AACTGGTGT TGAAGTTATC ATCCGTAAAA ACGGTTCTAC TGACATCTCT AACTGACA 960
ACTTCGTACG TAAAAACGAC CTGGCTTACA TCAACGTTGT TGACCGTGAC GTTGAATACC 1020
GTCTGTACGC TGACATCTCT ATCGCTAAAC CGGAAAAAAT CATCAAACTG ATCCGTACTT 1080
CTAACTCTAA CAACTCTCTG GGTCAGATCA TCGTTATGGA CTCGATCGGT AACAACTGCA 1140
CTATGAAGTT CCAGAACAAC AACGGTGGTA ACATCGGTCT GCTGGGTTTC CACTCTAACA 1200
ACCTGGTTGC TTCTTCTTGG TACTACAACA ACATCCGTAA AAACACTTCT TCTAACGGTT 1260
GCTTCTGGTC TTTCATCTCT AAAGAACACG GTTGGCAGGA AAATAATCT AGA 1313

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATCGAGGGAA GGATTTTCAGA ATTCGGATCC TCTAGAGTCG ACCTGCAGGC AAGCTTG

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(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ile Glu Gly Arg Ile
1 5

